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09/891,138	06/25/2001	Daniel Chi-Hong Lin	018781-006210US	8826

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EXAMINER

NICHOLS, CHRISTOPHER J

ART UNIT	PAPER NUMBER
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1647

DATE MAILED: 04/15/2003

13

Please find below and/or attached an Office communication concerning this application or proceeding.

**Office Action Summary**

Application No.

09/891,138

Applicant(s)

LIN ET AL.

Examiner

Christopher Nichols, Ph.D.

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

- 1) ☒ Responsive to communication(s) filed on 11 March 2003.
- 2a) ☐ This action is **FINAL**.                      2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

- 4) ☒ Claim(s) 1-3, 5-7, 13-18, 25-31 and 48-61 is/are pending in the application.
- 4a) Of the above claim(s) 25-29 and 48-61 is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1-3, 5-7, 13-18, 30, and 31 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

**Application Papers**

- 9) ☒ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
- Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
- 11) ☐ The proposed drawing correction filed on \_\_\_\_\_ is: a) ☐ approved b) ☐ disapproved by the Examiner.
- If approved, corrected drawings are required in reply to this Office action.
- 12) ☐ The oath or declaration is objected to by the Examiner.

**Priority under 35 U.S.C. §§ 119 and 120**

- 13) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- \* See the attached detailed Office action for a list of the certified copies not received.
- 14) ☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).
- a) ☐ The translation of the foreign language provisional application has been received.
- 15) ☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

**Attachment(s)**

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) 9, 10.
- 4) ☐ Interview Summary (PTO-413) Paper No(s). \_\_\_\_\_
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☐ Other: \_\_\_\_\_

## **DETAILED ACTION**

### ***Election/Restrictions***

1. Applicant's election **with** traverse of Group I (claims 1-18, 20, and 31) drawn to a G-protein coupled receptor encoded by the isolated nucleic acid comprising SEQ ID NO: 1 in Paper No. 12 (11 March 2003) is acknowledged. The traversal is on the ground(s) that search and examination of Groups I-V does not impose an undue burden. This is not found persuasive because Groups I-V are drawn to five distinct inventions each requiring a distinct and non-coextensive search of literature databases. In addition, as originally presented Groups I-V included 67 sequences, each independent and distinct thus requiring separate and non-coextensive searches of the sequence and literature databases. While it is understood that some sequences are linked structurally and functionally, the Examiner has examined the instant application to include BOTH SEQ ID NO: 1 and SEQ ID NO: 2, however, search and examination of the remaining 65 sequences would be an undue search burden on the Examiner. The requirement is still deemed proper and is therefore made FINAL.

### ***Status of Application, Amendments, and/or Claims***

2. The Preliminary Amendments of Paper No. 4 (09 January 2002), Paper No. 7 (15 July 2003), and Paper No. 12 (11 March 2003) has been received and entered in full. Claims 4, 8-12, 14, 19-24, 32-47, and 62-67 have been cancelled. Claims 1-3, 6-7, 13, 16-18, and 30 have been amended. Claims 1-3, 5-7, 13, 15-18, 30 and 31 are under examination.

***Specification***

3. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code (pp. 19 line 15). Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.
4. The disclosure is objected to because of the following informalities: define acronyms "TGR" and "EDG" (pp. 5 line 31). Appropriate correction is required.

***Claim Rejections - 35 USC § 101***

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

***Claim Rejections - 35 USC § 112***

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

5. Claims 1-3, 5-7, 13, 15-18, 30, and 31 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by a specific, substantial, and credible asserted utility or a well-established utility. The specification discloses the DNA sequence SEQ ID NO: 1 which encodes the polypeptide SEQ ID NO: 2. The specification asserts that the polypeptide SEQ ID NO: 2 is a novel G-protein coupled receptor (GPCR) expressed in the kidney. The claims are

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directed to isolated nucleic acid (SEQ ID NO: 1) encoding a polypeptide which is a member of the G-protein coupled receptor (GPCR) family comprising SEQ ID NO: 2. GPCRs are a gene superfamily known in the art to be expressed on the surface of many cell types and to encompass a massive receptor family. Gurrath [(2001) "Peptide-Binding G Protein-Coupled Receptors: New Opportunities for Drug Design" Current Medicinal Chemistry 8(13): 1605-1648] teaches that the GPCR superfamily constitutes the largest receptor family known. It is estimated that as many as 5000 distinct GPCR genes exist in the human genome. In addition, over 100 GPCRs are known with no characterized ligands and unknown physiological relevance (pp. 1606). Gurrath (2001) also teaches that all GPCRs are transmembrane receptors with a characteristic 7 transmembrane domain (TMD) motif, also known as "serpentine receptors", and all GPCRs work via a three-subunit effector system (pp. 1607; Figure 2). The state of the art holds that GPCRs fall into one of three major homology families for mammalian GPCRs: Family 1 (rho-family), Family 2 (scr-family), and Family 3 (metabotropic glutamate receptors) (pp. 1608-1609; Figure 4). Gurrath (2001) also teaches that GPCRs respond to a variety of agonists including but not limited to divalent cations, biogenic amines, fragrances, taste molecules, single amino acids, cannabinoids, prostaglandins, oligopeptides, globular proteins, chemokines, interleukins, neurotransmitters, and proteolytic enzymes (pp. 1609-1610; Table 1). The specification does not disclose any data for any activity for the polypeptide (SEQ ID NO: 2) encoded by SEQ ID NO: 1. There are no working examples.

6. There are no well-established utilities for newly discovered biological molecules.

However, the specification contains several assertions of utilities. Each will be discussed in turn.

a. *The nucleic acid SEQ ID NO: 1 encoded a is a novel GPCR (SEQ ID NO: 2):*

The Applicant's assertion that the polypeptide encoded by SEQ ID NO: 1 (SEQ ID NO: 2) is a GPCR is credible because it shares sequence homology with known GPCRs. However, this assertion is not specific, as the art recognizes a large number of GPCRs nor is it substantial. Firstly, it is not clear from the specification or the claims to which GPCR is claimed. For instance, US 6420137 B1 (16 July 2002) discloses that neurotensin receptors, a family of GPCRs, have three receptor subtypes: NT1R, NT2R, and NT3R. US 6420137 teaches that the subtypes, although similar in size have several sequence differences (Col. 4 line 35-61). Furthermore, NT1R shares only 43% sequence identity with NT2R while NT2R shares 79% sequence identity with NT3R (Col. 3 lines 5-50). In addition, despite being members of a single receptor family, NT1R, NT2R, and NT3R have different affinities for levocabastine, a ligand (Col. 3 lines 38-42). Secondly, the specification's assertion that SEQ ID NO: 2 is a novel GPCR is not a substantial assertion of utility, since significant further research would be required of the skilled artisan to determine what SEQ ID NO: 2's properties are. It is noted that US 6420137 performed binding and functional assays to confirm the identity of their putative NTRs (Col. 5 lines 28-50; Figure 1-3). It is noted, however, that the highest sequence homology (38.2% for SEQ ID NO: 1 and 74.3% for SEQ ID NO: 2) for both SEQ ID NO: 1 and SEQ ID NO: 2 is to purigenic receptors in US 5871963 [16 February 1999 (IDS)] and US 6063582 [16 May 2000 (IDS)]. Neither patent is drawn to a known GPCR. Also, US 5871963 and US 6063582 include functional assays of their novel receptors (Figure 3 in each patent).

b. *The polypeptide (SEQ ID NO: 2) encoded by SEQ ID NO: 1 has GPCR biological activity:* The specification asserts that SEQ ID NO: 2 is a GPCR, which based on its

structural similarity to prior art of GPCRs that have been characterized. While this assertion is credible it is neither specific nor substantial. It is not specific because this assertion would not have been accepted by one skilled in the art because the art establishes that GPCRs, while structurally similar, are functionally diverse. It is not substantial because of the lack of a working example of GPCR functional activity. The art teaches that using known and functionally established clones of GPCRs can yield genes of varying sequence homology. For instance, Howard et al. [(2001) "Orphan G-protein-coupled receptors and natural ligand discovery." TRENDS in Pharmacological Sciences 22(3): 132-140] teaches that the family of GPCR shares 7 TMD, and extracellular N-terminal domains, and intracellular-C-terminal domains with several conserved structural motifs. Despite this conservation of structural motifs, GPCRs usually only share ~45% sequence identity with one another. Furthermore, sequence homology is not indicative of which physiologically relevant ligands are active with a particular GPCR (pp. 132; Table 2). The assertion that SEQ ID NO: 2 is a GPCR is not substantial because the art acknowledges that function cannot be predicted based solely on structural similarity to a protein found in the sequence databases. For instance, Mazella et al. [(15 September 1996) "Structure, Functional Expression, and Cerebral Localization of the Levocabastine-Sensitive Neurotensin/Neuromedin N Receptor from Mouse Brain." The Journal of Neuroscience 16(18): 5613-5620] teaches that levocabastine-sensitive neurotensin (NT) receptor described therein shares 39% sequence homology to previously cloned NT receptors (pp. 5614). Mazella et al. teaches that despite being a GPCR and a member of the NT receptor family, the newly cloned

receptor has different pharmacological properties from other known NT receptors (pp. 5615; pp. 5618-5619; Table 1; Figure 4). Therefore sequence homology is not a reliable as the sole basis upon which to establish biological activity. For example, Skolnick et al. (2000, Trends in Biotech. 18:34-39) state that knowing the protein structure by itself is insufficient to annotate a number of functional classes, and is also insufficient for annotating the specific details of protein function (see Box 2, p. 36). Similarly, Bork (2000, Genome Research 10:398-400) states that the error rate of functional annotations in the sequence database is considerable, making it even more difficult to infer correct function from a structural comparison of a new sequence with a sequence database (see especially p. 399). Such concerns are also echoed by Doerks et al. (1998, Trends in Genetics 14:248-250) who state that (1) functional information is only partially annotated in the database, ignoring multi functionality, resulting in underpredictions of functionality of a new protein and (2) overpredictions of functionality occur because structural similarity often does not necessarily coincide with functional similarity. Smith et al. (1997, Nature Biotechnology 15:1222-1223) remarks that there are numerous cases in which proteins having very different functions share structural similarity due to evolution from a common ancestral gene. Brenner (1999, Trends in Genetics 15:132-133) argues that accurate inference of function from homology must be a difficult problem since, assuming there are only about 1000 major gene superfamilies in nature, then most homologs must have different molecular and cellular functions. Finally, Bork et al. (1996, Trends in Genetics 12:425-427) add that the software robots that assign functions to new proteins often assign a function to a whole new protein based on structural



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similarity of a small domain of the new protein to a small domain of a known protein. Such questionable interpretations are written into the sequence database and are then considered facts. In any case, the art clearly shows that structural similarity of different GPCRs is not predictive of expression patterns or functional similarity [Howard et al. 2001) Table 2]. For instance, Saria [(30 June 1999) "The tachykinin NK<sub>1</sub> receptor in the brain: pharmacology and putative functions." European Journal of Pharmacology 375(1-3): 51-60] despite high sequence homology (95%) between human and rat tachykinin NK<sub>1</sub> receptors (a GPCR), the different species isoforms show different binding properties to the same ligands (pp. 53-54 #6; Table 3). Therefore, the specification's assertion that SEQ ID NO: 1 encodes a polypeptide with GPCR activity is not a substantial assertion of utility, since significant further research would be required of the skilled artisan to determine what those activities are due the differences in sequence.

c. *The isolated nucleic acid (SEQ ID NO: 1) can be used to make a polypeptide (SEQ ID NO: 2) for analysis, characterization, or therapeutic uses:* This asserted utility is not substantial nor specific. In recombinately expressing a polypeptide, the polynucleotide is transfected into a host cell and then the protein is recovered. However, the instant specification does not disclose any known function for the claimed polypeptide or any disease state, toxin, or poison associated with SEQ ID NO: 1. In addition, this utility assertion is not specific as it can be applied to any given polynucleotide. Therefore, it is not clear how the skilled artisan would use a polypeptide manufactured by this method, for analysis, characterization, or therapeutic uses. Since

significant further research would be required to determine how to use the identified polynucleotide, the asserted utility is not substantial.

d. *The polypeptide (SEQ ID NO: 2) encoded by SEQ ID NO: 1 can be used to screen for a ligand:* The specification does not identify any specific ligands for the claimed novel GPCR. In respect to GPCRs, Kenakin [(2002) "Drug Efficacy at G Protein-Coupled Receptors" Annu. Rev. Pharmacol. Toxicol. 42: 349-379] teaches their binding and response to specific ligands (agonists) is variable, as are the effects on the receptor. In addition, receptor behavior involves several reactions including but not limited to internalization, pleiotropic interaction with multiple G-proteins, desensitization, oligomerization, and interaction with membrane auxiliary proteins (pp. 357; 362-367; Figure 1-4). For instance, US 6207799 (27 March 2001) teaches that different fragments of neuropeptide Y (NPY) and an analog, peptide YY (PYY), exhibit various affinities for the same peptide-neurotransmitter receptor, neuropeptide Y5 (Y5) (Col. 4 lines 46-65; Col. 14 lines 41-55; Table 1; Figure 1-2). This isoform only shares 30-33% sequence identity to the other neuropeptide Y receptors (Y1, Y2, and Y4) (Col. 4 lines 22-25). Further, each isoform of the neuropeptide Y receptor (Y1, Y2, Y4, Y5) has different binding properties for PYY, NPY, and its fragments (Table 2). Further, as noted above by Gurrath (2001) and Howard et al. (2001) possible GPCR ligands cover a huge range of bioactive molecules including but not limited to light,  $\text{Ca}^{2+}$ , odorants, amino acids, nucleotides, peptides, fatty acid derivatives, and polypeptide ligands (pp. 132). A skilled artisan would have had to experiment significantly to identify any allergy, disease, or disorder associated with SEQ ID NO: 2. Therefore, the asserted utility is not substantial.

The asserted utility is also not specific, since all receptors can be used to screen for ligands.

e. *SEQ ID NO: 1 is useful as a probe or primer:* The specification asserts that the isolated nucleic acid (SEQ ID NO: 1) is useful a probe to detect genes encoding SEQ ID NO: 1 or variants thereof, as primers to amplify corresponding gene fragments, to identify potential genetic disorders, in sequence arrays, to screen collections of genetic material from patients who have a particular medical condition, to make a cDNA library, to search sequence databases, to search cDNA libraries, or to identify mutations associated with a particular disease of SEQ ID NO: 1. This asserted utility is credible, but is neither substantial nor specific. Since there is no substantial utility for the encoded polypeptide, there is also no substantial utility for the nucleic acid probes to identify such. It would take significant further research to determine if the polynucleotide could be used as probes for particular diseases, since no nexus between a disease state and an alteration in SEQ ID NO: 1 expression levels or form (i.e. mutations) has been disclosed in the specification. Further, since all nucleic acids can be used as probes or primers, this asserted utility is not specific.

f. *The polypeptide encoded by SEQ ID NO: 1 does not have a known ligand:* The specification does not identify any specific ligands for the claimed GPCR that have been identified. A skilled artisan would have had to experiment significantly to identify any allergy, disease, or disorder associated with SEQ ID NO: 1. Therefore, the asserted utility is not substantial. The asserted utility is also not specific, since all receptors can be used to screen for ligands.

g. *The nucleic acid SEQ ID NO: 1 has therapeutic uses:* While this asserted utility is credible, it is neither specific nor substantial. The instant specification does not disclose any known disease state, toxin, or poison associated with SEQ ID NO: 1. Weiss [(May 1998) "G Protein-Coupled Receptor Signaling in the Kidney." Cell. Signal. 10(5): 313-320] teaches GPCRs in the kidney:

"...utilize different second-message molecules to transmit their signals to different functional units within renal cells. Inappropriate secretion of growth factors or constitutive activation of the corresponding receptors may lead to renal disease and arteriosclerosis. Furthermore, many renal disease and some systemic hypertension are the result of genetic defects that result in altered coupling of the G protein to the growth factor receptor or to downstream molecules." (pp. 318)

The instant specification does not elucidate as to the nature or molecular mechanism by which SEQ ID NO: 1 is involved in GPCR related kidney disease or disorders or offer any concrete guidance as to which disease or disorder SEQ ID NO: 1 is involved.

Therefore, it is not clear how the skilled artisan would use the polynucleotide for therapeutic uses. Since significant further research would be required to determine how to use the identified polynucleotide, the asserted utility is not substantial.

h. *The nucleic acid encoding (SEQ ID NO:1) and the polypeptide (SEQ ID NO: 2) can be recorded on computer readable media:* This asserted utility is not substantial.

The instant specification does not disclose any known disease state, toxin, or poison associated with SEQ ID NO: 1 or its activity. Therefore, it is not clear how the skilled artisan would use the computer readable media as identified by this method, for therapeutic or diagnostic uses. Since significant further research would be required to

determine how to use the identified nucleic acid or polypeptide, the asserted utility is not substantial.

i. *The claimed nucleic acid molecules can be used in assays for drug screening to identify compounds that modulate secreted protein nucleic acid expression:* This asserted utility is also not substantial. In such assays, compounds are screened for their ability to up-regulate or down-regulate expression of the nucleic acid molecule. Compounds that have on or the other activity are then labeled as potential drugs. However, the instant specification does not disclose any specific disease state wherein there is a change in SEQ ID NO: 1 expression levels or forms (i.e., mutations). Therefore, it is not clear how the skilled artisan would use a potential drug identified by this method. Since significant further research would be required to determine how to use the identified potential drugs, the asserted utility is not substantial.

7. Therefore, in the absence of a well-established utility, and the absence of a specific, substantial and credible asserted utility, the claimed invention lacks patentable utility under 35 U.S.C. § 101.

8. **If Applicant can submit evidence (in the form of a declaration under 37 CFR 1.132 or post-filing date publications) supporting the specification's assertion that SEQ ID NO: 1 encodes a polypeptide (SEQ ID NO: 1) that has a specific function similar to a known G-protein coupled receptor, wherein the specific function was predicted by the specification as originally filed, such would be viewed favorably as evidence of patentable utility.**

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9. Claims 1-3, 5-7, 13, 15-18, 30, and 31 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a credible, specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

10. Furthermore regarding variants and fragments of SEQ ID NO: 2 polypeptides, the problem of predicting protein structure from sequence data and in turn utilizing predicted structural determinations to ascertain functional aspects of the protein is extremely complex.

While it is known that many amino acid substitutions are generally possible in any given protein the positions within the protein's sequence where such amino acid substitutions can be made with a reasonable expectation of success are limited. Certain positions in the sequence are critical to the protein's structure/function relationship, e.g. such as various sites or regions directly involved in binding, activity and in providing the correct three-dimensional spatial orientation of binding and active sites. These or other regions may also be critical determinants of antigenicity. These regions can tolerate only relatively conservative substitutions or no substitutions (see Wells, 1990, Biochemistry 29:8509-8517; Ngo et al., 1994, The Protein Folding Problem and Tertiary Structure Prediction, pp. 492-495). However, Applicant has provided little or no guidance beyond the mere presentation of sequence data to enable one of ordinary skill in the art to determine, without undue experimentation, the positions in the protein which are tolerant to change (e.g. such as by amino acid substitutions or deletions), and the nature and extent of changes that can be made in these positions. Although the specification outlines art-recognized procedures for producing and screening for active muteins, this is not adequate guidance as to the nature of active derivatives that may be constructed, but is merely an invitation to the artisan to

use the current invention as a starting point for further experimentation. Even if an active or binding site were identified in the specification, they may not be sufficient, as the ordinary artisan would immediately recognize that an active or binding site must assume the proper three-dimensional configuration to be active, which conformation is dependent upon surrounding residues; therefore substitution of non-essential residues can often destroy activity. The art recognizes that function cannot be predicted from structure alone (Bork, 2000, *Genome Research* 10:398-400; Skolnick et al., 2000, *Trends in Biotech.* 18(1): 34-39, especially p. 36 at Box 2; Doerks et al., 1998, *Trends in Genetics* 14:248-250; Smith et al., 1997, *Nature Biotechnology* 15:1222-1223; Brenner, 1999, *Trends in Genetics* 15:132-133; Bork et al., 1996, *Trends in Genetics* 12:425-427). Due to the large quantity of experimentation necessary to generate the infinite number of derivatives recited in the claims and possibly screen same for activity, the lack of direction/guidance presented in the specification regarding which structural features are required in order to provide activity, the absence of working examples directed to same, the complex nature of the invention, the state of the prior art which establishes the unpredictability of the effects of mutation on protein structure and function, and the breadth of the claims which fail to recite any structural or functional limitations, undue experimentation would be required of the skilled artisan to make and/or use the claimed invention in its full scope.

11. Claims 1-3, 5-7, 13, 15-18, 30, and 31 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The specification does not contain a written description of variants and fragments of the claimed GPCR.

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12. *Vas-Cath Inc. v. Mahurkar*, 19USPQ2d 1111, clearly states that “applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of *the invention*. The invention is, for purposes of the ‘written description’ inquiry, *whatever is now claimed*.” (See page 1117.) The specification does not “clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed.” (See *Vas-Cath* at page 1116).

13. With the exception of SEQ ID NO: 1 and SEQ ID NO: 2, the skilled artisan cannot envision the detailed chemical structure of the encompassed polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

14. One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF’s were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

15. Therefore, only isolated polypeptides comprising the amino acid sequence set forth in SEQ ID NO: 2 as encoded by SEQ ID NO: 1, but not the full breadth of the claim meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).



16. Claim 18 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The term "stringency" in claim 18 is a relative term which renders the claim indefinite. The term "stringency" is not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the scope of the invention. Neither the specification nor the art defines the term unambiguously. Thus the metes and bounds of the claims cannot be determined.

*Summary*

17. Claims 1-3, 5-7, 13-18, 30 and 31 are hereby rejected.

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***Conclusion***

Any inquiry concerning this communication or earlier communications from the examiner should be directed to **Christopher Nichols, Ph.D.** whose telephone number is 703-305-3955. The examiner can normally be reached on Monday through Friday, 8:30AM to 5:00PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, **Gary Kunz, Ph.D.** can be reached on 703-308-4623. The fax phone numbers for the organization where this application or proceeding is assigned are 703-872-9306 for regular communications and 703-872-9307 for After Final communications. The fax phone numbers for the customer service center is 703-872-9305.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 703-308-0196.

CJN  
April 8<sup>th</sup>, 2003

*Elizabeth C. Kemmerer*

**ELIZABETH KEMMERER  
PRIMARY EXAMINER**